REMARKS

Upon entry of the foregoing amendments, allowed claims 33, 34 and 49-52, and currently rejected claims 53-58 will be pending in the application. Claims 33, 53 and 56 are independent claims.

Independent claims 53 and 56 have been amended to more particularly point out and distinctly claim the subject matter which Applicants regard as their rejection. The amendments recite that the isolated protein of each claim is not a full length NhhA polypeptide. This is supported by the application as originally filed. The invention has always excluded full length NhhA polypeptides. See, for example, page 3, lines 1-6. These claims have also been amended to use the proper italics for the microorganism *N. meningitides*. Since no new matter has been added by the amendments, their entry is respectfully solicited.

Applicants traverse the rejection of claims 53-59 for the following reasons.

35 USC §112, First Paragraph - Enablement

The Examiner has stated at page 7 of the Office Action that claims 53-58 do not comply with section 112, first paragraph, reiterating that this is an enablement rejection. The Examiner has asserted, in essence summarizing this rejection: "Applicant has shown how to make and use SEQ ID NOS:23 and 35 but has not shown how to make variants of the polypeptides as set forth in SEQ ID NOS:23 and 35 that retain the same functional properties." [Original emphasis].

With respect, the specification has always provided variants of these sequences and how to make and use them.

The following tables show the level of sequence identity between SEQ ID NOS:23 and 35 and other isolated proteins set forth in the specification as originally filed. The comparisons are based on ClustalW (v. 1.4) program sequence alignments, within the MacVector sequence analysis package. Copies of the printouts on which the tables are based are submitted with this Amendment.

Comparison	% identity

4

SEQ ID NO: 23 vs 24	95
SEQ ID NO: 23 vs 25	79
SEQ ID NO: 23 vs 26	84
SEQ ID NO: 23 vs 27	93
SEQ ID NO: 23 vs 35	90
SEQ ID NO: 23 vs 36	85
SEQ ID NO: 23 vs 37	69
SEQ ID NO: 23 vs 38	74
SEQ ID NO: 23 vs 39	84

Comparison	% identity
SEQ ID NO: 35 vs 23	90
SEQ ID NO: 35 vs 24	85
SEQ ID NO: 35 vs 25	79
SEQ ID NO: 35 vs 26	93
SEQ ID NO: 35 vs 27	85
SEQ ID NO: 35 vs 36	95
SEQ ID NO: 35 vs 37	77
SEQ ID NO: 35 vs 38	82
SEQ ID NO: 35 vs 39	93

Applicants submit that the high level of sequence identity between many of these sequences (generally 79%-95%) support the levels of identity recited by claims 53 and 56. These are all proteins engineered to provide cross-strain immunity to *N. meningitidis*. They all share a deletion of most or all of the V1 region and in some cases, deletion of other V regions. Thus, Applicants respectfully contend that they fall squarely within the ambit of "variants," in the words of the Examiner. Therefore, Applicants submit that they have indeed provided a representative number of species within the claimed genus of polypeptides and, accordingly, that we have shown how to make variants of the polypeptides as set forth in SEQ ID NOS:23 and 35.

Also at page 7 of the Office Action, the Examiner has commented on Figure 1 and Table 1 of the specification as "merely disclosing conserved regions and variable regions...which are used to generate a consensus sequence.... Figure 1 and Table 1 in no way convey which amino acids are modified...."

With respect, while Table 1 indeed discloses conserved and variable regions, claims 23 and 35 are not predicated on, or restricted to, isolated proteins which are modified by amino acid sequence modification (*e.g.* by substitution). A very large number of protein sequences having at least 80% or 90% sequence identity to SEQ ID NO:23 or 35 can be made by replacing, deleting and/or shuffling V and/or C regions, with a view to creating a protein that elicits a more cross-protective immune response. This is a process well within the capabilities of a person of ordinary skill in the art armed with Table 1.

Notwithstanding this ability, Figure 1 indeed shows which modifications to make to thereby ensure that a protein can be made that is less strain-specific or more cross-protective.

Figure 1 indicates residue-by-residue, for each of SEQ ID NOS:1-10, the variations that can occur. This information can be readily applied to SEQ ID NO:23 and SEQ ID NO:35, because these sequences are derived from SEQ ID NO: 1.

In some cases, residues are absolutely conserved between SEQ ID NOS:1-10 (*e.g.* residue 62 L); in some cases, a limited set of variations occurs between SEQ ID NOS:1-10 (*e.g.* residue 72 G or L); in some cases, a more extensive set of variations occurs between SEQ ID NOS:1-10 (*e.g.* residue 106 G, R, A or I); and in some cases certain residues may be present or absent between SEQ ID NOS:1-10 (*e.g.* residue 57 may be E or entirely absent).

This requires no guesswork or undue experimentation. The variations are all spelled out in FIG. 1.

This is very useful guidance to enable a skilled person to decide which amino acids of SEQ ID NO:23 or SEQ ID NO:35 can be deleted (*e.g.* residues that vary considerably between SEQ ID NOS:1-10 or are not always present in SEQ ID NOS:1-10) to maximize cross-protection. Furthermore, Figure 1 allows the identification of modifications that retain relatively invariant residues, or substitutions of an amino acid residue with another residue that is typically present in one or more of SEQ ID NOS:1-10, to thereby maximize cross-protection.

In summary, the specification provides more than an adequate representative number of species of the genus of proteins encompassed by claims 53-58. Furthermore, sufficient, explicit guidance is provided by Table 1, Figure 1 and the specification in general to readily enable a skilled

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person to make amino acid sequence modifications that fall within the ambit of claims 53-58. The variants clearly would be used in substantially the same way as SEQ ID NOS:23 and 35.

Applicants therefore submit that the enablement rejection of claims 53-58 as currently amended is no appropriate. Favorable reconsideration and withdrawal of these rejections are respectfully solicited.

35 USC §102 (a) - Novelty
Masignani

The Examiner has cited Masignani as disclosing a protein sequence (SEQ ID NO:4 of Masignani) that allegedly has over 98% identity to SEQ ID NO: 23 and at least 98% sequence identity to SEQ ID NO:35.

Applicants submit that claims 53-58 are *prima facie* novel over Masignani by virtue of the recitation in claims 53 and 56 that the isolated protein is not a full length NhhA polypeptide. In contrast, SEQ ID NO:4 of Masignani is a full length NhhA polypeptide.

Applicants respectfully question how the Examiner arrived at the alleged levels of identity specified in this rejection, as their own analysis reveals substantially less identity.

Claims 53 and 56 recite that the at least 80% or 90% identity is compared across the entire length of the protein relative to SEQ ID NOS:35 or 23, respectively.

SEQ ID NO:23 has a deletion (compared to the full length NhhA polypeptide of SEQ ID NO:1) of residues 55-133 (see Example 4). SEQ ID NO:1 is the same sequence as SEQ ID NO:4 of Masignani. This is a significant deletion.

A ClustalW comparison of SEQ ID NO:23 with SEQ ID NO:4 of Masignani reveals only about 86% identity over the entire sequences. A copy of a printout based on this comparison is enclosed with this Amendment. This clearly is outside the scope of claim 56, and further distinguishes the subject matter of claims 56-58 from Masignani.

SEQ ID NO:35 has a further 51 amino acid deletion (compared to the full length NhhA polypeptide of SEQ ID NO:1) due to N-terminal processing (see Example 4).

A ClustalW comparison of SEQ ID NO:35 with SEQ ID NO:4 of Masignani reveals only 77% identity over the entire sequences. A printout of the analysis is enclosed with this Amendment. This is outside the scope of both of claims 53-58, and further distinguishes the claimed proteins from Masignani.

In view of the data presented with the enclosures to this Amendment, Applicants cannot understand how the 98% level of identity with Masignani is arrived at by the Examiner.

Nevertheless, as pointed out above, the sequences encompassed by claims 53-58 are not full length NhhA polypeptides, such as SEQ ID NO:4 of Masignani and exclude from their scope sequences such as SEQ ID NO:4 of Masignani.

Peak

The Examiner has cited Peak as disclosing a protein sequence (SEQ ID NO:2 of Peak) that allegedly has over 98% identity to SEQ ID NO: 23 and at least 99% sequence identity to SEQ ID NO:35.

Applicants submit that claims 53-58 are *prima facie* novel over Peak by virtue of the recitations in claims 53 and 56 that the isolated protein is not a full length NhhA polypeptide. In contrast, SEQ ID NO:2 of Peak <u>is</u> a full length NhhA polypeptide.

Moreover, as with Masignani, Applicants question how the Examiner arrived at the alleged levels of identity compared to Peak specified in this rejection.

Claims 53 and 56 recite that the at least 80% or 90% identity is compared across the <u>entire</u> length of the protein relative to SEQ ID NOS:35 or 23, respectively. SEQ ID NO:23 has a deletion (compared to the full length NhhA polypeptide of SEQ ID NO:1) of residues 55-133 (see Example 4).

SEQ ID NO:1 in the present application is 99.6% identical to SEQ ID NO:2 of Peak.

A ClustalW comparison of SEQ ID NO:23 with SEQ ID NO:2 of Peak reveals only about 86% identity over the <u>entire</u> sequences. A printout based on this comparison is enclosed with this Amendment. This is outside the scope of claim 56, and further distinguishes claims 56-58 from Peak.

SEQ ID NO:35 has a further 51 amino acid deletion (compared to a full length NhhA polypeptide) due to N-terminal processing (see Example 4).

A ClustalW comparison of SEQ ID NO:35 with SEQ ID NO:2 of Peak reveals only 77% identity over the <u>entire</u> sequences. A printout based on this comparison is enclosed with this Amendment. This is outside the scope of all of claims 53-58.

In view of the data presented with the enclosures to this Amendment, Applicants cannot understand how the 98% - 99% level of identity with Peak is arrived at by the Examiner.

Nevertheless, as pointed out above, the sequences encompassed by claims 53-58 are not full length NhhA polypeptides, such as SEQ ID NO:2 of Peak and exclude from their scope sequences such as SEQ ID NO:2 of Peak.

In view of the significant distinctions between the claimed invention on the one hand and Masignani and Peak on the other hand, Applicants respectfully submit that the novelty rejection under section 102(a) is moot and request favorable reconsideration and withdrawal of these prior art rejections. Moreover, the cited prior art would not render the subject matter of these claims obvious.

While Applicants appreciate the prior indication of allowability of claims 33, 34 and 49-52, reconsideration and withdrawal of all of the rejections of claims 53-58 and an early Notice of Allowance relating to all claims are respectfully solicited.

Respectfully submitted,

IAN RICHARD ANSELM PEAK *et al.*

December 6, 2006   By: _____
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ASN:hg
Enclosures

7657446 v1

US App. 09/771,382 Alignments of SEQ ID Nos: 23-27 and 35-39

Attached are documents that provide the sequences for alignment in US App.
09/771,382.

The purpose is:

(a)   to determine the % identity between SEQ ID NO:23 and all other
      sequences provided in the list
(b)   to determine the % identity between SEQ ID NO:35 and all other
      sequences provided in the list

This includes determining the % identity between SEQ ID NO:23 and SEQ ID
NO:35.

The determination should be over the entire length of each protein.

Results:

SEQ ID NO	23	24	25	26	27	35	36	37	38	39
23	100%	95%	79%	84%	93%	90%	85%	69%	74%	84%
35	90%	85%	79%	84%	85%	100%	95%	77%	82%	93%

Comparisons were done using ClustalW, within the MacVector sequence
analysis package. Alignments, details of parameters used and comparisons are
detailed in the attached pages.

SEQ ID NO:23

```
MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS ANNETDLTSV      60
GTEKLSFSAN GNKVNITSDT KGLNFAKETA GTNGDTTVHL NGIGSTLTDT LLNTGATTNV     120
TNDNVTDDEK KRAASVKDVL NAGWNIKGVK PGTTASDNVD FVRTYDTVEF LSADTKTTTV     180
NVESKDNGKK TEVKIGAKTS VIKEKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK     240
AGWRMKTTTA NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA     300
LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI     360
ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK EGDVTNVAQL     420
KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS     480
SISDGGNWII KGTASGNSRG HFGASASVGY QW
```

SEQ ID NO:24

```
MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN ATDETGLINV      60
ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL NGIGSTLTDM LLNTGATTNV     120
TNDNVTDDEK KRAASVKDVL NAGWNIKGVK PGTTASDNVD FVRTYDTVEF LSADTKTTTV     180
NVESKDNGKK TEVKIGAKTS VIKEKDGKLV TGKGKGENGS STDEGEGLVT AKEVIDAVNK     240
AGWRMKTTTA NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA     300
LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI     360
ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP VRITNVAPGV KEGDVTNVAQ     420
LKGVAQNLNN RIDNVNGNAR AGIAQAIATA GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY     480
SSISAGGNWI IKGTASGNSR GHFGASASVG YQW                                 513
```

SEQ ID NO:25

```
MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS ANNVDFVRTY      60
DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK DGKLVTGKDK GENGSSTDEG     120
EGLVTAKEVI DAVNKAGWRM KTTTANGQTG QADKFETVTS GTNVTFASGK GTTATVSKDD     180
QGNITVMYDV NVGDALNVNQ LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA     240
GNNIEITRNG KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV     300
APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY LPGKSMMAIG     360
GGTYRGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS ASVGYQW                  407
```

SEQ ID NO:26

```
MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS ANRAASVKDV      60
LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT VNVESKDNGK KTEVKIGAKT     120
SVIKEKDGKL VTGKDKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK     180
FETVTSGTNV TFASGKGTTA TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA     240
GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA     300
PTLSVDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVDGNAR     360
AGIAQAIATA GLVQAYLPGK SMMAIGGGTY RGEAGYAIGY SSISDGGNWI IKGTASGNSR     420
GHFGASASVG YQW                                                      433
```

SEQ ID NO:27

```
MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS ANTLKAGDNL      60
KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN     120
GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK     180
TEVKIGAKTS VIKEKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA     240
NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG     300
WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI ATSMTPQFSS     360
VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK EGDVTNVAQL KGVAQNLNNR     420
IDNVDGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII     480
KGTASGNSRG HFGASASVGY QW
```

SEQ ID NO:35

```
NNETDLTSVG  TEKLSFSANG  NKVNITSDTK  GLNFAKETAG  TNGDTTVHLN  GIGSTLTDTL       60
LNTGATTNVT  NDNVTDDEKK  RAASVKDVLN  AGWNIKGVKP  GTTASDNVDF  VRTYDTVEFL      120
SADTKTTTVN  VESKDNGKKT  EVKIGAKTSV  IKEKDGKLVT  GKDKGENGSS  TDEGEGLVTA      180
KEVIDAVNKA  GWRMKTTTAN  GQTGQADKFE  TVTSGTNVTF  ASGKGTTATV  SKDDQGNITV      240
MYDVNVGDAL  NVNQLQNSGW  NLDSKAVAGS  SGKVISGNVS  PSKGKMDETV  NINAGNNIEI      300
TRNGKNIDIA  TSMTPQFSSV  SLGAGADAPT  LSVDGDALNV  GSKKDNKPVR  ITNVAPGVKE      360
GDVTNVAQLK  GVAQNLNNRI  DNVDGNARAG  IAQAIATAGL  VQAYLPGKSM  MAIGGGTYRG      420
EAGYAIGYSS  ISDGGNWIIK  GTASGNSRGH  FGASASVGYQ  W
```

SEQ ID NO:36

```
TDETGLINVE  TEKLSFGANG  KKVNIISDTK  GLNFAKETAG  TNGDTTVHLN  GIGSTLTDML       60
LNTGATTNVT  NDNVTDDEKK  RAASVKDVLN  AGWNIKGVKP  GTTASDNVDF  VRTYDTVEFL      120
SADTKTTTVN  VESKDNGKKT  EVKIGAKTSV  IKEKDGKLVT  GKGKGENGSS  TDEGEGLVTA      180
KEVIDAVNKA  GWRMKTTTAN  GQTGQADKFE  TVTSGTKVTF  ASGNGTTATV  SKDDQGNITV      240
KYDVNVGDAL  NVNQLQNSGW  NLDSKAVAGS  SGKVISGNVS  PSKGKMDETV  NINAGNNIEI      300
TRNGKNIDIA  TSMTPQFSSV  SLGAGADAPT  LSVDDEGALN  VGSKDANKPV  RITNVAPGVK      360
EGDVTNVAQL  KGVAQNLNNR  IDNVNGNARA  GIAQAIATAG  LVQAYLPGKS  MMAIGGGTYL      420
GEAGYAIGYS  SISAGGNWII  KGTASGNSRG  HFGASASVGY  QW                         462
```

SEQ ID NO:37

```
NNVDFVRTYD  TVEFLSADTK  TTTVNVESKD  NGKKTEVKIG  AKTSVIKEKD  GKLVTGKDKG       60
ENGSSTDEGE  GLVTAKEVID  AVNKAGWRMK  TTTANGQTGQ  ADKFETVTSG  TNVTFASGKG      120
TTATVSKDDQ  GNITVMYDVN  VGDALNVNQL  QNSGWNLDSK  AVAGSSGKVI  SGNVSPSKGK      180
MDETVNINAG  NNIEITRNGK  NIDIATSMTP  QFSSVSLGAG  ADAPTLSVDG  DALNVGSKKD      240
NKPVRITNVA  PGVKEGDVTN  VAQLKGVAQN  LNNRIDNVDG  NARAGIAQAI  ATAGLVQAYL      300
PGKSMMAIGG  GTYRGEAGYA  IGYSSISDGG  NWIIKGTASG  NSRGHFGASA  SVGYQW          356
```

SEQ ID NO:38

```
NRAASVKDVL  NAGWNIKGVK  PGTTASDNVD  FVRTYDTVEF  LSADTKTTTV  NVESKDNGKK       60
TEVKIGAKTS  VIKEKDGKLV  TGKDKGENGS  STDEGEGLVT  AKEVIDAVNK  AGWRMKTTTA      120
NGQTGQADKF  ETVTSGTNVT  FASGKGTTAT  VSKDDQGNIT  VMYDVNVGDA  LNVNQLQNSG      180
WNLDSKAVAG  SSGKVISGNV  SPSKGKMDET  VNINAGNNIE  ITRNGKNIDI  ATSMTPQFSS      240
VSLGAGADAP  TLSVDGDALN  VGSKKDNKPV  RITNVAPGVK  EGDVTNVAQL  KGVAQNLNNR      300
IDNVDGNARA  GIAQAIATAG  LVQAYLPGKS  MMAIGGGTYR  GEAGYAIGYS  SISDGGNWII      360
KGTASGNSRG  HFGASASVGY  QW
```

SEQ ID NO:39

```
S ANTLKAGDNLKIKQFTYSLK  KDLTDLTSVG  TEKLSFSANG  NKVNITSDTK  GLNFAKETAG
TNGDTTVHLN  GIGSTLTDRA  ASVKDVLNAG  WNIKGVKNVD  FVRTYDTVEF  LSADTKTTTV
NVESKDNGKK  TEVKIGAKTS  VIKEKDGKLV  TGKDKGENGS  STDEGEGLVT  AKEVIDAVNK
AGWRMKTTTA  NGQTGQADKF  ETVTSGTNVT  FASGKGTTAT  VSKDDQGNIT  VMYDVNVGDA
LNVNQLQNSG  WNLDSKAVAG  SSGKVISGNV  SPSKGKMDET  VNINAGNNIE  ITRNGKNIDI
ATSMTPQFSS  VSLGAGADAP  TLSVDGDALN  VGSKKDNKPV  RITNVAPGVK  EGDVTNVAQL
KGVAQNLNNR  IDNVDGNARA  GIAQAIATAG  LVQAYLPGKS  MMAIGGGTYR  GEAGYAIGYS
SISDGGNWII  KGTASGNSRG  HFGASASVGY  QW
```

of 2

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2831
Gaps Inserted = 1   Conserved Identities = 489

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.4 seconds

1. SEQ ID NO 23 vs. SEQ ID NO 24
   _____

    Aligned Length = 513   Gaps = 1
    Identities = 489 (95%)   Similarities = 1 (0%)

```
SEQ ID NO 23    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS   50
SEQ ID NO 24    1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQAN   50
                  **************** ***************************** ***

SEQ ID NO 23   51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL  100
SEQ ID NO 24   51 ATDETGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHL  100
                  * . **  *  * ****** *** ****  *********************

SEQ ID NO 23  101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK  150
SEQ ID NO 24  101 NGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK  150
                  ********* ***************************************

SEQ ID NO 23  151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  200
SEQ ID NO 24  151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  200
                  *************************************************

SEQ ID NO 23  201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA  250
SEQ ID NO 24  201 VIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA  250
                  ************* ***********************************

SEQ ID NO 23  251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA  300
SEQ ID NO 24  251 NGQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDA  300
                  ***************** ****** ***************** *******

SEQ ID NO 23  301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE  350
SEQ ID NO 24  301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE  350
                  *************************************************

SEQ ID NO 23  351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKKDNKP  399
SEQ ID NO 24  351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKP  400
                  ********************************** *** ******  ***

SEQ ID NO 23  400 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATA  449
SEQ ID NO 24  401 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATA  450
                  *********************************** *************

SEQ ID NO 23  450 GLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSR  499
SEQ ID NO 24  451 GLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSR  500
                  ******************** ************** ************
```

```
SEQ ID NO 23   500 GHFGASASVGYQW 512
SEQ ID NO 24   501 GHFGASASVGYQW 513
                   *************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2374
Gaps Inserted = 1   Conserved Identities = 407

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 23 vs. SEQ ID NO 25</u>

    Aligned Length = 512   Gaps = 1
    Identities = 407 (79%)   Similarities = 0 (0%)

```
SEQ ID NO 23     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID NO 25     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
                   *************************************************


SEQ ID NO 23    51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 100
SEQ ID NO 25    51 AN-----------------------------------------------  52
                   **


SEQ ID NO 23   101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 150
SEQ ID NO 25    53 -------------------------------------------------  52


SEQ ID NO 23   151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 200
SEQ ID NO 25    53 -------NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  95
                          ******************************************


SEQ ID NO 23   201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 250
SEQ ID NO 25    96 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 145
                   *************************************************


SEQ ID NO 23   251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 300
SEQ ID NO 25   146 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 195
                   *************************************************


SEQ ID NO 23   301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 350
SEQ ID NO 25   196 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 245
                   *************************************************


SEQ ID NO 23   351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 400
SEQ ID NO 25   246 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 295
                   *************************************************


SEQ ID NO 23   401 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 450
SEQ ID NO 25   296 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 345
                   *************************************************


SEQ ID NO 23   451 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 500
SEQ ID NO 25   346 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 395
                   *************************************************
```

```
SEQ ID NO 23  501 HFGASASVGYQW 512
SEQ ID NO 25  396 HFGASASVGYQW 407
                  ************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2530
Gaps Inserted = 1   Conserved Identities = 433

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. SEQ ID NO 23 vs. SEQ ID NO 26

    Aligned Length = 512   Gaps = 1
    Identities = 433 (84%)   Similarities = 0 (0%)

```
SEQ ID NO 23    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID NO 26    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
                  *************************************************


SEQ ID NO 23   51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 100
SEQ ID NO 26   51 AN------------------------------------------------  52
                  **


SEQ ID NO 23  101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 150
SEQ ID NO 26   53 ---------------------------RAASVKDVLNAGWNIKGVK  71
                                             ******************


SEQ ID NO 23  151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 200
SEQ ID NO 26   72 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 121
                  *************************************************


SEQ ID NO 23  201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 250
SEQ ID NO 26  122 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 171
                  *************************************************


SEQ ID NO 23  251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 300
SEQ ID NO 26  172 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 221
                  *************************************************


SEQ ID NO 23  301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 350
SEQ ID NO 26  222 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 271
                  *************************************************


SEQ ID NO 23  351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 400
SEQ ID NO 26  272 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 321
                  *************************************************


SEQ ID NO 23  401 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 450
SEQ ID NO 26  322 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 371
                  *************************************************


SEQ ID NO 23  451 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 500
SEQ ID NO 26  372 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 421
                  *************************************************
```

$\text{q}2$

```
SEQ ID NO 23  501 HFGASASVGYQW 512
SEQ ID NO 26  422 HFGASASVGYQW 433
                  ************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2819
Gaps Inserted = 3   Conserved Identities = 481

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.4 seconds

1. <u>SEQ ID NO 23 vs. SEQ ID NO 27</u>

    Aligned Length = 531   Gaps = 3
    Identities = 481 (93%)   Similarities = 0 (0%)

```
SEQ ID NO 23     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID NO 27     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
                   **************************************************


SEQ ID NO 23    51 AN-------------------NETDLTSVGTEKLSFSANGNKVNITSDTK  81
SEQ ID NO 27    51 ANTLKAGDNLKIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTK 100
                   **                   *************************


SEQ ID NO 23    82 GLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKK 131
SEQ ID NO 27   101 GLNFAKETAGTNGDTTVHLNGIGSTLTD--------------------- 128
                   ***************************


SEQ ID NO 23   132 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVN 181
SEQ ID NO 27   129 RAASVKDVLNAGWNIKGVK-------NVDFVRTYDTVEFLSADTKTTTVN 171
                   *******************       ************************


SEQ ID NO 23   182 VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA 231
SEQ ID NO 27   172 VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA 221
                   **************************************************


SEQ ID NO 23   232 KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 281
SEQ ID NO 27   222 KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 271
                   **************************************************


SEQ ID NO 23   282 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 331
SEQ ID NO 27   272 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 321
                   **************************************************


SEQ ID NO 23   332 PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPT 381
SEQ ID NO 27   322 PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPT 371
                   **************************************************


SEQ ID NO 23   382 LSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRI 431
SEQ ID NO 27   372 LSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRI 421
                   **************************************************


SEQ ID NO 23   432 DNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSS 481
SEQ ID NO 27   422 DNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSS 471
                   **************************************************
```

```
SEQ ID NO 23  482 ISDGGNWIIKGTASGNSRGHFGASASVGYQW 512
SEQ ID NO 27  472 ISDGGNWIIKGTASGNSRGHFGASASVGYQW 502
                  ******************************
```

of 2

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2681
Gaps Inserted = 0   Conserved Identities = 461

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.4 seconds

1. <u>SEQ ID NO 23 vs. SEQ ID NO 35</u>

    Aligned Length = 512   Gaps = 0
    Identities = 461 (90%)   Similarities = 0 (0%)

```
SEQ ID NO 23     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS   50
SEQ ID NO 35     1                                                         0


SEQ ID NO 23    51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL  100
SEQ ID NO 35     1 NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL   49
                   *************************************************

SEQ ID NO 23   101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK  150
SEQ ID NO 35    50 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK   99
                   **************************************************

SEQ ID NO 23   151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  200
SEQ ID NO 35   100 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  149
                   **************************************************

SEQ ID NO 23   201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA  250
SEQ ID NO 35   150 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA  199
                   **************************************************

SEQ ID NO 23   251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA  300
SEQ ID NO 35   200 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA  249
                   **************************************************

SEQ ID NO 23   301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE  350
SEQ ID NO 35   250 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE  299
                   **************************************************

SEQ ID NO 23   351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV  400
SEQ ID NO 35   300 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV  349
                   **************************************************

SEQ ID NO 23   401 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG  450
SEQ ID NO 35   350 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG  399
                   **************************************************

SEQ ID NO 23   451 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG  500
SEQ ID NO 35   400 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG  449
                   **************************************************
```

```
SEQ ID NO 23  501 HFGASASVGYQW 512
SEQ ID NO 35  450 HFGASASVGYQW 461
                  ************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2554
Gaps Inserted = 1   Conserved Identities = 440

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 23 vs. SEQ ID NO 36</u>

    Aligned Length = 513   Gaps = 1
    Identities = 440 (85%)   Similarities = 1 (0%)

```
SEQ ID NO 23    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID NO 36    1                                                     0


SEQ ID NO 23   51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 100
SEQ ID NO 36    1  TDETGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHL  49
                   . ** *   * ****** *** **** *********************

SEQ ID NO 23  101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 150
SEQ ID NO 36   50 NGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK  99
                   ********* ***************************************

SEQ ID NO 23  151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 200
SEQ ID NO 36  100 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 149
                   *************************************************

SEQ ID NO 23  201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 250
SEQ ID NO 36  150 VIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 199
                   ************* ***********************************

SEQ ID NO 23  251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 300
SEQ ID NO 36  200 NGQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDA 249
                   ***************** ****** **************** ********

SEQ ID NO 23  301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 350
SEQ ID NO 36  250 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 299
                   *************************************************

SEQ ID NO 23  351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKKDNKP 399
SEQ ID NO 36  300 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKP 349
                   ·**********************************  *******  ***

SEQ ID NO 23  400 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATA 449
SEQ ID NO 36  350 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATA 399
                   *********************************** *************

SEQ ID NO 23  450 GLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSR 499
SEQ ID NO 36  400 GLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSR 449
                   ******************** ************** **************
```

SEQ ID NO 23   500 GHFGASASVGYQW 512
SEQ ID NO 36   450 GHFGASASVGYQW 462
               ****

ɗ 2

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2075
Gaps Inserted = 0   Conserved Identities = 355

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. SEQ ID NO 23 vs. SEQ ID NO 37

    Aligned Length = 512   Gaps = 0
    Identities = 355 (69%)   Similarities = 0 (0%)

```
SEQ ID NO 23    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID NO 37    1                                                     0


SEQ ID NO 23   51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 100
SEQ ID NO 37    1                                                     0


SEQ ID NO 23  101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 150
SEQ ID NO 37    1                                                     0


SEQ ID NO 23  151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 200
SEQ ID NO 37    1         NNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  44
                           ****************************************


SEQ ID NO 23  201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 250
SEQ ID NO 37   45 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA  94
                  *************************************************


SEQ ID NO 23  251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 300
SEQ ID NO 37   95 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 144
                  *************************************************


SEQ ID NO 23  301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 350
SEQ ID NO 37  145 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 194
                  *************************************************


SEQ ID NO 23  351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 400
SEQ ID NO 37  195 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 244
                  *************************************************


SEQ ID NO 23  401 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 450
SEQ ID NO 37  245 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 294
                  *************************************************


SEQ ID NO 23  451 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 500
SEQ ID NO 37  295 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 344
                  *************************************************
```

```
SEQ ID NO 23  501 HFGASASVGYQW 512
SEQ ID NO 37  345 HFGASASVGYQW 356
                  ************
```

of 2

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2229
Gaps Inserted = 0   Conserved Identities = 381

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 23 vs. SEQ ID NO 38</u>

    Aligned Length = 512   Gaps = 0
    Identities = 381 (74%)   Similarities = 0 (0%)

```
SEQ ID NO 23     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID NO 38     1                                                      0


SEQ ID NO 23    51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 100
SEQ ID NO 38     1                                                      0


SEQ ID NO 23   101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 150
SEQ ID NO 38     1                             NRAASVKDVLNAGWNIKGVK  20
                                                ********************

SEQ ID NO 23   151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 200
SEQ ID NO 38    21 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  70
                   *************************************************

SEQ ID NO 23   201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 250
SEQ ID NO 38    71 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 120
                   *************************************************

SEQ ID NO 23   251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 300
SEQ ID NO 38   121 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 170
                   *************************************************

SEQ ID NO 23   301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 350
SEQ ID NO 38   171 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 220
                   *************************************************

SEQ ID NO 23   351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 400
SEQ ID NO 38   221 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 270
                   *************************************************

SEQ ID NO 23   401 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 450
SEQ ID NO 38   271 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 320
                   *************************************************

SEQ ID NO 23   451 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 500
SEQ ID NO 38   321 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 370
                   *************************************************
```

```
SEQ ID NO 23   501 HFGASASVGYQW 512
SEQ ID NO 38   371 HFGASASVGYQW 382
                   ************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2510
Gaps Inserted = 2   Conserved Identities = 432

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 23 vs. SEQ ID NO 39</u>

    Aligned Length = 512   Gaps = 2
    Identities = 432 (84%)   Similarities = 3 (0%)

```
SEQ ID NO 23     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID NO 39     1                           SANTLKAGDNLKIKQFTYSL  20
                                              **.    *       .        .


SEQ ID NO 23    51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 100
SEQ ID NO 39    21 KKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL  70
                      *************************************************


SEQ ID NO 23   101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 150
SEQ ID NO 39    71 NGIGSTLTD--------------------RAASVKDVLNAGWNIKGVK  98
                      *********                    ******************


SEQ ID NO 23   151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 200
SEQ ID NO 39    99 -------NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 141
                          *****************************************


SEQ ID NO 23   201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 250
SEQ ID NO 39   142 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 191
                      *************************************************


SEQ ID NO 23   251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 300
SEQ ID NO 39   192 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 241
                      *************************************************


SEQ ID NO 23   301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 350
SEQ ID NO 39   242 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 291
                      *************************************************


SEQ ID NO 23   351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 400
SEQ ID NO 39   292 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 341
                      *************************************************


SEQ ID NO 23   401 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 450
SEQ ID NO 39   342 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 391
                      *************************************************


SEQ ID NO 23   451 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 500
SEQ ID NO 39   392 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 441
                      *************************************************
```

SEQ ID NO 23   501 HFGASASVGYQW 512
SEQ ID NO 39   442 HFGASASVGYQW 453
                   ****

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2681
Gaps Inserted = 0   Conserved Identities = 461

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.4 seconds

1. SEQ ID NO 35 vs. SEQ ID NO 23

    Aligned Length = 512   Gaps = 0
    Identities = 461 (90%)   Similarities = 0 (0%)

```
SEQ ID NO 35    1                                                    0
SEQ ID NO 23    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50


SEQ ID NO 35    1  NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL  49
SEQ ID NO 23   51 ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 100
                   *************************************************

SEQ ID NO 35   50 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK  99
SEQ ID NO 23  101 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 150
                  **************************************************

SEQ ID NO 35  100 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 149
SEQ ID NO 23  151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 200
                  **************************************************

SEQ ID NO 35  150 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 199
SEQ ID NO 23  201 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA 250
                  **************************************************

SEQ ID NO 35  200 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 249
SEQ ID NO 23  251 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA 300
                  **************************************************

SEQ ID NO 35  250 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 299
SEQ ID NO 23  301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 350
                  **************************************************

SEQ ID NO 35  300 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 349
SEQ ID NO 23  351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 400
                  **************************************************

SEQ ID NO 35  350 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 399
SEQ ID NO 23  401 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 450
                  **************************************************

SEQ ID NO 35  400 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 449
SEQ ID NO 23  451 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 500
                  **************************************************
```

```
SEQ ID NO 35   450 HFGASASVGYQW 461
SEQ ID NO 23   501 HFGASASVGYQW 512
                   ************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2554
Gaps Inserted = 1   Conserved Identities = 440

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. SEQ ID NO 35 vs. SEQ ID NO 24

    Aligned Length = 513   Gaps = 1
    Identities = 440 (85%)   Similarities = 1 (0%)

```
SEQ ID NO 35    1                                                    0
SEQ ID NO 24    1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQAN  50


SEQ ID NO 35    1 NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL   49
SEQ ID NO 24   51 ATDETGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHL 100
                  .  ** *   *  ****** *** ****  **********************

SEQ ID NO 35   50 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK   99
SEQ ID NO 24  101 NGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK  150
                  ********* *****************************************

SEQ ID NO 35  100 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  149
SEQ ID NO 24  151 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS  200
                  ***************************** ********************

SEQ ID NO 35  150 VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA  199
SEQ ID NO 24  201 VIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA  250
                  ************* ************************************

SEQ ID NO 35  200 NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA  249
SEQ ID NO 24  251 NGQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDA  300
                  ***************** ****** ***************** *******

SEQ ID NO 35  250 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE  299
SEQ ID NO 24  301 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE  350
                  **************************************************

SEQ ID NO 35  300 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKKDNKP  348
SEQ ID NO 24  351 ITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKP  400
                  ***********************************    ******   ***

SEQ ID NO 35  349 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATA  398
SEQ ID NO 24  401 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATA  450
                  *********************************** **************

SEQ ID NO 35  399 GLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSR  448
SEQ ID NO 24  451 GLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSR  500
                  ******************** ************** **************
```

of 2

```
SEQ ID NO 35   449 GHFGASASVGYQW 461
SEQ ID NO 24   501 GHFGASASVGYQW 513
                   *************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2138
Gaps Inserted = 2   Conserved Identities = 367

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 35 vs. SEQ ID NO 25</u>

    Aligned Length = 461   Gaps = 2
    Identities = 367 (79%)   Similarities = 11 (2%)

```
SEQ ID NO 35     1 NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN  50
SEQ ID NO 25     1                                                  MN   2
                                                                    .*

SEQ ID NO 35    51 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 100
SEQ ID NO 25     3 KIYRIIWNSALNAWVVVSELTRNHT---KRASATVKTAVLATLLFATVQA  49
                   *    .  .**.      .  * *   *. .*.**  .  *       *.

SEQ ID NO 35   101 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV 150
SEQ ID NO 25    50 S---ANNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV  96
                   .   *********************************************

SEQ ID NO 35   151 IKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 200
SEQ ID NO 25    97 IKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 146
                   *************************************************

SEQ ID NO 35   201 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDAL 250
SEQ ID NO 25   147 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDAL 196
                   *************************************************

SEQ ID NO 35   251 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 300
SEQ ID NO 25   197 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 246
                   *************************************************

SEQ ID NO 35   301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 350
SEQ ID NO 25   247 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 296
                   *************************************************

SEQ ID NO 35   351 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL 400
SEQ ID NO 25   297 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL 346
                   *************************************************

SEQ ID NO 35   401 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH 450
SEQ ID NO 25   347 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH 396
                   *************************************************

SEQ ID NO 35   451 FGASASVGYQW 461
SEQ ID NO 25   397 FGASASVGYQW 407
                   **********
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2264
Gaps Inserted = 2   Conserved Identities = 391

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 35 vs. SEQ ID NO 26</u>

    Aligned Length = 473   Gaps = 2
    Identities = 391 (84%)   Similarities = 4 (0%)

```
SEQ ID NO 35    1            NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKET   38
SEQ ID NO 26    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRAS--ATVKTAVLATLLFATVQ   48
                            *    . *  *    .  *      *.    * **


SEQ ID NO 35   39 AGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDV   88
SEQ ID NO 26   49 ASAN------------------------------------RAASVKDV   60
                  *  .*                                    *******


SEQ ID NO 35   89 LNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK  138
SEQ ID NO 26   61 LNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK  110
                  **************************************************


SEQ ID NO 35  139 KTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVN  188
SEQ ID NO 26  111 KTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVN  160
                  **************************************************


SEQ ID NO 35  189 KAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNI  238
SEQ ID NO 26  161 KAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNI  210
                  **************************************************


SEQ ID NO 35  239 TVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE  288
SEQ ID NO 26  211 TVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE  260
                  **************************************************


SEQ ID NO 35  289 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDAL  338
SEQ ID NO 26  261 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDAL  310
                  **************************************************


SEQ ID NO 35  339 NVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNAR  388
SEQ ID NO 26  311 NVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNAR  360
                  **************************************************


SEQ ID NO 35  389 AGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI  438
SEQ ID NO 26  361 AGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI  410
                  **************************************************


SEQ ID NO 35  439 IKGTASGNSRGHFGASASVGYQW  461
SEQ ID NO 26  411 IKGTASGNSRGHFGASASVGYQW  433
                  ***********************
```

ⅅ2

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2518
Gaps Inserted = 2   Conserved Identities = 429

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 35 vs. SEQ ID NO 27</u>

    Aligned Length = 531   Gaps = 2
    Identities = 429 (85%)   Similarities = 0 (0%)

```
SEQ ID NO 35   1                                                    0
SEQ ID NO 27   1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50


SEQ ID NO 35   1                         NNETDLTSVGTEKLSFSANGNKVNITSDTK  30
SEQ ID NO 27  51 ANTLKAGDNLKIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTK 100
                                       **************************

SEQ ID NO 35  31 GLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKK  80
SEQ ID NO 27 101 GLNFAKETAGTNGDTTVHLNGIGSTLTD--------------------- 128
                 **************************

SEQ ID NO 35  81 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVN 130
SEQ ID NO 27 129 RAASVKDVLNAGWNIKGVK-------NVDFVRTYDTVEFLSADTKTTTVN 171
                 *******************       ************************

SEQ ID NO 35 131 VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA 180
SEQ ID NO 27 172 VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA 221
                 *************************************************

SEQ ID NO 35 181 KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 230
SEQ ID NO 27 222 KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 271
                 *************************************************

SEQ ID NO 35 231 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 280
SEQ ID NO 27 272 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 321
                 *************************************************

SEQ ID NO 35 281 PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPT 330
SEQ ID NO 27 322 PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPT 371
                 *************************************************

SEQ ID NO 35 331 LSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRI 380
SEQ ID NO 27 372 LSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRI 421
                 *************************************************

SEQ ID NO 35 381 DNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSS 430
SEQ ID NO 27 422 DNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSS 471
                 *************************************************
```

```
SEQ.ID NO 35   431 ISDGGNWIIKGTASGNSRGHFGASASVGYQW 461
SEQ ID NO 27   472 ISDGGNWIIKGTASGNSRGHFGASASVGYQW 502
                   ******************************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2544
Gaps Inserted = 1   Conserved Identities = 440

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 35 vs. SEQ ID NO 36</u>

    Aligned Length = 462   Gaps = 1
    Identities = 440 (95%)   Similarities = 1 (0%)

SEQ ID NO 35   1 NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 50
SEQ ID NO 36   1 TDETGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 50
                   . ** * * ****** *** **** ************************

SEQ ID NO 35   51 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 100
SEQ ID NO 36   51 GIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 100
                   ******** **

SEQ ID NO 35   101 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV 150
SEQ ID NO 36   101 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV 150
                   ****

SEQ ID NO 35   151 IKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 200
SEQ ID NO 36   151 IKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 200
                   ************ ************************************

SEQ ID NO 35   201 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDAL 250
SEQ ID NO 36   201 GQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDAL 250
                   **************** ****** **************** *********

SEQ ID NO 35   251 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 300
SEQ ID NO 36   251 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 300
                   ****

SEQ ID NO 35   301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKKDNKPV 349
SEQ ID NO 36   301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV 350
                   ********************************** ******* ****

SEQ ID NO 35   350 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 399
SEQ ID NO 36   351 RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAG 400
                   ********************************** ***************

SEQ ID NO 35   400 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG 449
SEQ ID NO 36   401 LVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRG 450
                   ******************* ************* ***************

SEQ ID NO 35   450 HFGASASVGYQW 461
SEQ ID NO 36   451 HFGASASVGYQW 462
                   ****

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2075
Gaps Inserted = 0   Conserved Identities = 355

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 35 vs. SEQ ID NO 37</u>

    Aligned Length = 461   Gaps = 0
    Identities = 355 (77%)   Similarities = 0 (0%)

```
SEQ ID NO 35     1 NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN  50
SEQ ID NO 37     1                                                        0


SEQ ID NO 35    51 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 100
SEQ ID NO 37     1                                                        0


SEQ ID NO 35   101 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV 150
SEQ ID NO 37     1       NNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV  45
                         *********************************************

SEQ ID NO 35   151 IKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 200
SEQ ID NO 37    46 IKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN  95
                   *************************************************

SEQ ID NO 35   201 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDAL 250
SEQ ID NO 37    96 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDAL 145
                   *************************************************

SEQ ID NO 35   251 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 300
SEQ ID NO 37   146 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 195
                   *************************************************

SEQ ID NO 35   301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 350
SEQ ID NO 37   196 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 245
                   *************************************************

SEQ ID NO 35   351 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL 400
SEQ ID NO 37   246 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL 295
                   *************************************************

SEQ ID NO 35   401 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH 450
SEQ ID NO 37   296 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH 345
                   *************************************************

SEQ ID NO 35   451 FGASASVGYQW 461
SEQ ID NO 37   346 FGASASVGYQW 356
                   ***********
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2229
Gaps Inserted = 0   Conserved Identities = 381

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 35 vs. SEQ ID NO 38</u>

    Aligned Length = 461   Gaps = 0
    Identities = 381 (82%)   Similarities = 0 (0%)

```
SEQ ID NO 35    1 NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN  50
SEQ ID NO 38    1                                                      0


SEQ ID NO 35   51 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 100
SEQ ID NO 38    1                            NRAASVKDVLNAGWNIKGVKP  21
                                             *******************


SEQ ID NO 35  101 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV 150
SEQ ID NO 38   22 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV  71
                  *************************************************


SEQ ID NO 35  151 IKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 200
SEQ ID NO 38   72 IKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 121
                  *************************************************


SEQ ID NO 35  201 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDAL 250
SEQ ID NO 38  122 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDAL 171
                  *************************************************


SEQ ID NO 35  251 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 300
SEQ ID NO 38  172 NVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI 221
                  *************************************************


SEQ ID NO 35  301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 350
SEQ ID NO 38  222 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 271
                  *************************************************


SEQ ID NO 35  351 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL 400
SEQ ID NO 38  272 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL 321
                  *************************************************


SEQ ID NO 35  401 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH 450
SEQ ID NO 38  322 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH 371
                  *************************************************


SEQ ID NO 35  451 FGASASVGYQW 461
SEQ ID NO 38  372 FGASASVGYQW 382
                  **********
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2518
Gaps Inserted = 2   Conserved Identities = 429

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. <u>SEQ ID NO 35 vs. SEQ ID NO 39</u>

    Aligned Length = 482   Gaps = 2
    Identities = 429 (93%)   Similarities = 0 (0%)

```
SEQ ID NO 35    1                     NNETDLTSVGTEKLSFSANGNKVNITSDT   29
SEQ ID NO 39    1 SANTLKAGDNLKIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDT   50
                                      *************************


SEQ ID NO 35   30 KGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEK   79
SEQ ID NO 39   51 KGLNFAKETAGTNGDTTVHLNGIGSTLTD--------------------   79
                  ****************************


SEQ ID NO 35   80 KRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTV  129
SEQ ID NO 39   80 -RAASVKDVLNAGWNIKGVK-------NVDFVRTYDTVEFLSADTKTTTV  121
                   ******************        **********************


SEQ ID NO 35  130 NVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVT  179
SEQ ID NO 39  122 NVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVT  171
                  *************************************************


SEQ ID NO 35  180 AKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTAT  229
SEQ ID NO 39  172 AKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTAT  221
                  *************************************************


SEQ ID NO 35  230 VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNV  279
SEQ ID NO 39  222 VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNV  271
                  *************************************************


SEQ ID NO 35  280 SPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP  329
SEQ ID NO 39  272 SPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP  321
                  *************************************************


SEQ ID NO 35  330 TLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNR  379
SEQ ID NO 39  322 TLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNR  371
                  *************************************************


SEQ ID NO 35  380 IDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYS  429
SEQ ID NO 39  372 IDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYS  421
                  *************************************************


SEQ ID NO 35  430 SISDGGNWIIKGTASGNSRGHFGASASVGYQW  461
SEQ ID NO 39  422 SISDGGNWIIKGTASGNSRGHFGASASVGYQW  453
                  *******************************
```

SEQUENCE COMPARISONS Masignani WO99/36544 vs. US App. 09/771,382

A: Peak US 6,197,312 SEQ ID NO:2 = SEQ ID NO:4 of Masignani

```
MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS ANNEEQEEDL      60
YLDPVQRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK GVLTAREITL KAGDNLKIKQ     120
NGTNFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN     180
GIGSTLTDTL LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVKP GTTASDNVDF     240
VRTYDTVEFL SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGKLVT GKDKGENGSS     300
TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF ASGKGTTATV     360
SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS SGKVISGNVS PSKGKMDETV     420
NINAGNNIEI TRNGKNIDIA TSMTPQFSSV SLGAGADAPT LSVDGDALNV GSKKDNKPVR     480
ITNVAPGVKE GDVTNVAQLK GVAQNLNNRI DNVDGNARAG IAQAIATAGL VQAYLPGKSM     540
MAIGGGTYRG EAGYAIGYSS ISDGGNWIIK GTASGNSRGH FGASASVGYQ W             591
```

B: SEQ ID NO:23 of US App. 09/771,382

```
MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS ANNETDLTSV      60
GTEKLSFSAN GNKVNITSDT KGLNFAKETA GTNGDTTVHL NGIGSTLTDT LLNTGATTNV     120
TNDNVTDDEK KRAASVKDVL NAGWNIKGVK PGTTASDNVD FVRTYDTVEF LSADTKTTTV     180
NVESKDNGKK TEVKIGAKTS VIKEKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK     240
AGWRMKTTTA NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA     300
LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI     360
ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK EGDVTNVAQL     420
KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS     480
SISDGGNWII KGTASGNSRG HFGASASVGY QW
```

C: SEQ ID NO:35 of US App. 09/771,382

```
NNETDLTSVG TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL      60
LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVKP GTTASDNVDF VRTYDTVEFL     120
SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGKLVT GKDKGENGSS TDEGEGLVTA     180
KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF ASGKGTTATV SKDDQGNITV     240
MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS SGKVISGNVS PSKGKMDETV NINAGNNIEI     300
TRNGKNIDIA TSMTPQFSSV SLGAGADAPT LSVDGDALNV GSKKDNKPVR ITNVAPGVKE     360
GDVTNVAQLK GVAQNLNNRI DNVDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG     420
EAGYAIGYSS ISDGGNWIIK GTASGNSRGH FGASASVGYQ W
```

1

Run comparisons to determine % identity:

    B vs A
    C vs A

Alignments carried out using "clustalW".

ClustalW (v1.4) multiple sequence alignment

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2976
Gaps Inserted = 1   Conserved Identities = 512

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
  Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1
  Similarity Matrix: id

Multiple Alignment Parameters:
  Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1
  Delay Divergent = 40% Gap Distance = 8
  Similarity Matrix: id

Processing time: 0.7 seconds

```
B      1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS   50
A      1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS   50
         *************************************************

B     51 ANNE--------------------------------------------   54
A     51 ANNEEQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEK  100
         ****

B     55 ------------------------------TDLTSVGTEKLSFSANG   71
A    101 GVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANG  150
                                       ****************

B     72 NKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVT  121
A    151 NKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVT  200
         *************************************************

B    122 NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL  171
A    201 NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL  250
         *************************************************

B    172 SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS  221
A    251 SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS  300
         *************************************************

B    222 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF  271
A    301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF  350
```

```
      *********************************************

B  272  ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS  321
A  351  ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS  400
      *********************************************

B  322  SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV  371
A  401  SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV  450
      *********************************************


B  372  SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLK  421
A  451  SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLK  500
      *********************************************

B  422  GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG  471
A  501  GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG  550
      *********************************************

B  472  EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW  512
A  551  EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW  591
      *****************************************
```

% identity = 512 conserved identities/591 amino acids = 86.6%

3

Option 1 (no gaps in C)
ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2663
Gaps Inserted = 0   Conserved Identities = 458

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.6 seconds

1. C vs. A

    Aligned Length = 591   Gaps = 0
    Identities = 458 (77%)   Similarities = 0 (0%)


```
C     1 --------------------------------------------------   0
A     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50


C     1 --------------------------------------------------   0
A    51 ANNEEQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEK 100


C     1 -----------------------------NNETDLTSVGTEKLSFSANG  20
A   101 GVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANG 150
                                       ****************

C    21 NKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVT  70
A   151 NKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVT 200
         *************************************************

C    71 NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL 120
A   201 NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL 250
         *************************************************

C   121 SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 170
A   251 SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 300
         *************************************************

C   171 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 220
A   301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 350
         *************************************************

C   221 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS 270
A   351 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS 400
```

4

```
          ****************************************************

C  271  SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV  320
A  401  SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV  450
          ****************************************************


C  321  SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLK  370
A  451  SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLK  500
          ****************************************************


C  371  GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG  420
A  501  GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG  550
          ****************************************************


C  421  EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW  461
A  551  EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW  591
          *****************************************
```

Option 2 (manual alignment, gap in C
ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2691
Gaps Inserted = 1   Conserved Identities = 461

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.2
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.6 seconds

1. C vs. A

    Aligned Length = 591   Gaps = 1
    Identities = 461 (78%)   Similarities = 0 (0%)

C   1 -- 0
A   1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS 50

C   1 -NNE-- 3
A   51 ANNEEQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEK 100
        ***

C   4 -----------------------------TDLTSVGTEKLSFSANG 20
A   101 GVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANG 150
                                     ****

C   21 NKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVT 70
A   151 NKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVT 200
        ****

C   71 NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL 120
A   201 NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL 250
        ****

C   121 SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 170
A   251 SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 300
        ****

C   171 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 220
A   301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 350
        ****

C   221 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS 270
A   351 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS 400
        ****

```
C  271  SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV  320
A  401  SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV  450
        *************************************************

C  321  SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLK  370
A  451  SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLK  500
        *************************************************

C  371  GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG  420
A  501  GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG  550
        *************************************************

C  421  EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW  461
A  551  EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW  591
        *****************************************
```

SEQUENCE COMPARISONS Peak US Patent 6,197,312 vs. US App. 09/771,382

Attached are documents that provide the sequences for alignment.

The purpose is:
(a) to determine the % identity between Peak SEQ ID NO:2 and SEQ ID NO:23 &
(b) to determine the % identity between Peak SEQ ID NO:2 and SEQ ID NO:35.

The determination should be over the entire length of each protein.

    (a) = 86% (see attached pages 2 vs 23.pdf)
    (b) = 77% (see attached pages 2 vs 35.pdf)

Peak US Patent 6,197,312
SEQ ID NO:2

```
MNKIYRIIWN  SALNAWVVVS  ELTRNHTKRA  SATVKTAVLA  TLLFATVQAS  ANNERPRKKD      60
LYLDPVQRTV  AVLIVNSDKE  GTGEKEKVEE  NSDWAVYFNE  KGVLTAREIT  KAGDNLKIKQ     120
NGTNFTYSLK  KDLTDLTSVG  TEKLSFSANG  NKVNITSDTK  GLNFAKETAG  TNGDTTVHLN     180
GIGSTLTDTL  LNTGATTNVT  NDNVTDDEKK  RAASVKDVLN  AGWNIKGVKP  GTTASDNVDF     240
VRTYDTVEFL  SADTKTTTVN  VESKDNGKKT  EVKIGAKTSV  IKEKDGKLVT  GKDKGENGSS     300
TDEGEGLVTA  KEVIDAVNKA  GWRMKTTTAN  GQTGQADKFE  TVTSGTNVTF  ASGKGTTATV     360
SKDDQGNITV  MYDVNVGDAL  NVNQLQNSGW  NLDSKAVAGS  SGKVISGNVS  PSKGKMDETV     420
NINAGNNIEI  TRNGKNIDIA  TSMTPQFSSV  SLGAGADAPT  LSVDGDALNV  GSKKDNKPVR     480
ITNVAPGVKE  GDVTNVAQLK  GVAQNLNNRI  DNVDGNARAG  IAQAIATAGL  VQAYLPGKSM     540
MAIGGGTYRG  EAGYAIGYSS  ISDGGNWIIK  GTASGNSRGH  FGASASVGYQ  W
```

US App. 09/771,382
SEQ ID NO:23

```
MNKIYRIIWN  SALNAWVVVS  ELTRNHTKRA  SATVKTAVLA  TLLFATVQAS  ANNETDLTSV      60
GTEKLSFSAN  GNKVNITSDT  KGLNFAKETA  GTNGDTTVHL  NGIGSTLTDT  LLNTGATTNV     120
TNDNVTDDEK  KRAASVKDVL  NAGWNIKGVK  PGTTASDNVD  FVRTYDTVEF  LSADTKTTTV     180
NVESKDNGKK  TEVKIGAKTS  VIKEKDGKLV  TGKDKGENGS  STDEGEGLVT  AKEVIDAVNK     240
AGWRMKTTTA  NGQTGQADKF  ETVTSGTNVT  FASGKGTTAT  VSKDDQGNIT  VMYDVNVGDA     300
LNVNQLQNSG  WNLDSKAVAG  SSGKVISGNV  SPSKGKMDET  VNINAGNNIE  ITRNGKNIDI     360
ATSMTPQFSS  VSLGAGADAP  TLSVDGDALN  VGSKKDNKPV  RITNVAPGVK  EGDVTNVAQL     420
KGVAQNLNNR  IDNVDGNARA  GIAQAIATAG  LVQAYLPGKS  MMAIGGGTYR  GEAGYAIGYS     480
SISDGGNWII  KGTASGNSRG  HFGASASVGY  QW
```

US App. 09/771,382
SEQ ID NO:35

```
NNETDLTSVG  TEKLSFSANG  NKVNITSDTK  GLNFAKETAG  TNGDTTVHLN  GIGSTLTDTL      60
LNTGATTNVT  NDNVTDDEKK  RAASVKDVLN  AGWNIKGVKP  GTTASDNVDF  VRTYDTVEFL     120
SADTKTTTVN  VESKDNGKKT  EVKIGAKTSV  IKEKDGKLVT  GKDKGENGSS  TDEGEGLVTA     180
KEVIDAVNKA  GWRMKTTTAN  GQTGQADKFE  TVTSGTNVTF  ASGKGTTATV  SKDDQGNITV     240
MYDVNVGDAL  NVNQLQNSGW  NLDSKAVAGS  SGKVISGNVS  PSKGKMDETV  NINAGNNIEI     300
TRNGKNIDIA  TSMTPQFSSV  SLGAGADAPT  LSVDGDALNV  GSKKDNKPVR  ITNVAPGVKE     360
GDVTNVAQLK  GVAQNLNNRI  DNVDGNARAG  IAQAIATAGL  VQAYLPGKSM  MAIGGGTYRG     420
EAGYAIGYSS  ISDGGNWIIK  GTASGNSRGH  FGASASVGYQ  W
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2968
Gaps Inserted = 1   Conserved Identities = 511

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. SEQ ID 2 vs. SEQ ID 23

    Aligned Length = 592   Gaps = 1
    Identities = 511 (86%)   Similarities = 0 (0%)

```
SEQ ID 2    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID 23   1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
              **************************************************

SEQ ID 2   51 ANNERPRKKDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNE 100
SEQ ID 23  51 ANN----------------------------------------------  53
              ***

SEQ ID 2  101 KGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSAN 150
SEQ ID 23  54 ------------------------------ETDLTSVGTEKLSFSAN  70
                                            ***************

SEQ ID 2  151 GNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNV 200
SEQ ID 23  71 GNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNV 120
              **************************************************

SEQ ID 2  201 TNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF 250
SEQ ID 23 121 TNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF 170
              **************************************************

SEQ ID 2  251 LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 300
SEQ ID 23 171 LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 220
              **************************************************

SEQ ID 2  301 STDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVT 350
SEQ ID 23 221 STDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVT 270
              **************************************************

SEQ ID 2  351 FASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAG 400
SEQ ID 23 271 FASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAG 320
              **************************************************

SEQ ID 2  401 SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSS 450
SEQ ID 23 321 SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSS 370
              **************************************************

SEQ ID 2  451 VSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQL 500
SEQ ID 23 371 VSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQL 420
              **************************************************
```

```
SEQ ID 2   501 KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYR 550
SEQ ID 23  421 KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYR 470
               **************************************************

SEQ ID 2   551 GEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 592
SEQ ID 23  471 GEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 512
               *****************************************
```

ClustalW (v1.4) multiple sequence alignment

2 Sequences Aligned   Alignment Score = 2683
Gaps Inserted = 1   Conserved Identities = 460

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: id

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: id

Processing time: 0.3 seconds

1. SEQ ID 2 vs. SEQ ID 35

    Aligned Length = 592   Gaps = 1
    Identities = 460 (77%)   Similarities = 0 (0%)

```
SEQ ID 2     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS  50
SEQ ID 35    1                                                     0


SEQ ID 2    51 ANNERPRKKDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNE 100
SEQ ID 35    1 NN----------------------------------------------   2
               **

SEQ ID 2   101 KGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSAN 150
SEQ ID 35    3 ------------------------------ETDLTSVGTEKLSFSAN  19
                                             ***************

SEQ ID 2   151 GNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNV 200
SEQ ID 35   20 GNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNV  69
               *************************************************

SEQ ID 2   201 TNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF 250
SEQ ID 35   70 TNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF 119
               *************************************************

SEQ ID 2   251 LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 300
SEQ ID 35  120 LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 169
               *************************************************

SEQ ID 2   301 STDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVT 350
SEQ ID 35  170 STDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVT 219
               *************************************************

SEQ ID 2   351 FASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAG 400
SEQ ID 35  220 FASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAG 269
               *************************************************

SEQ ID 2   401 SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSS 450
SEQ ID 35  270 SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSS 319
               *************************************************

SEQ ID 2   451 VSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQL 500
SEQ ID 35  320 VSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQL 369
               *************************************************
```

```
SEQ ID 2   501 KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYR 550
SEQ ID 35  370 KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYR 419
               *************************************************

SEQ ID 2   551 GEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 592
SEQ ID 35  420 GEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 461
               ******************************************
```